RAW SEQUENCE LISTING ERROR REPORT
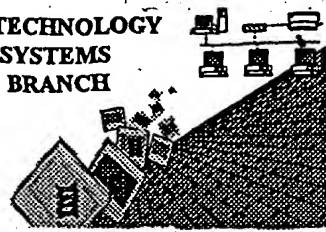
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/763,129A

Source: PCT09

Date Processed by STIC: 4/9/02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>, **EFS Submission User Manual - ePAVE**)
2. **U.S. Postal Service:** U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. **Hand Carry directly to:**
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
   Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED   SUGGESTED CORRECTION   SERIAL NUMBER: 09/763,129A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
      Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
      prevent "wrapping."

2_____Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3_____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
      Numbering   use space characters, instead.

4_____Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
      ensure your subsequent submission is saved in ASCII text.

5_____Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules,
      each n or Xaa can only represent a single residue. Please present the maximum number of each
      residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
      "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
      previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
      the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
      Artificial or Unknown sequences.

7_____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
      (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
      (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
      (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
      This sequence is intentionally skipped

      Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
      (NEW RULES)   <210> sequence id number
      <400> sequence id number
      000

9_____Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
      (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
      In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ___Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
      Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
      is Artificial Sequence

11_____Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
      Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
      "Unknown." Please explain source of genetic material in <220> to <223> section.
      (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12_____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
      "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
      listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____Misuse of n   n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent
      any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

Does Not Comply   PCT09
Corrected Diskette Needed

Errors on pp. 3-5

RAW SEQUENCE LISTING   DATE: 04/09/2002
PATENT APPLICATION: US/09/763,129A   TIME: 12:29:23

Input Set : **A:\EP.txt**
Output Set: **N:\CRF3\04092002\I763129A.raw**

```
 3 <110> APPLICANT: CO, MAN SUNG
 4         MAXIMILLIANO, VASQUEZ
 6 <120> TITLE OF INVENTION: ANTITHROMBOTIC AGENT AND HUMANIZED ANTI-VON WILLEBRAND
FACTOR MONOCLONAL
 7         ANTIBODY
 9 <130> FILE REFERENCE: 202617US0PCT
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/763,129A
C--> 12 <141> CURRENT FILING DATE: 2001-05-16
14 <150> PRIOR APPLICATION NUMBER: PCT/US99/16724
15 <151> PRIOR FILING DATE: 1999-08-19
17 <150> PRIOR APPLICATION NUMBER: 09/136,315
18 <151> PRIOR FILING DATE: 1998-08-19
20 <160> NUMBER OF SEQ ID NOS: 8
22 <170> SOFTWARE: PatentIn version 3.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 417
26 <212> TYPE: DNA
27 <213> ORGANISM: Mus musculus
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)..(417)
32 <223> OTHER INFORMATION:
35 <400> SEQUENCE: 1
36 atg gat ttt ggg ctg att ttt ttt att gtt gct ctt tta aaa ggg gtc      48
37 Met Asp Phe Gly Leu Ile Phe Phe Ile Val Ala Leu Leu Lys Gly Val
38 1               5                   10                  15
40 cag tgt gag gtg aaa ctt ctc gag tct gga ggt ggc ctg gtg cag act      96
41 Gln Cys Glu Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Thr
42              20                  25                  30
44 gga gga tcc ctg aaa ctc tcc tgt gca gcc tca gga ttc gat ttt agt     144
45 Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser
46          35                  40                  45
48 aga ttc tgg atg agt tgg gtc cgg cag gct cca ggg aaa ggg cta gaa     192
49 Arg Phe Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
50      50                  55                  60
52 tgg att gga gaa gtt aat cca gat aac aat acg atg aac tat acg cca     240
53 Trp Ile Gly Glu Val Asn Pro Asp Asn Asn Thr Met Asn Tyr Thr Pro
54 65                  70                  75                  80
56 tct cta aag gat aaa ttc atc atc tcc aga gac aac gcc aaa aat acg     288
57 Ser Leu Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr
58              85                  90                  95
60 ctg tac ctg caa atg agt caa gtg aga tct gag gac aca gcc ctt tac     336
61 Leu Tyr Leu Gln Met Ser Gln Val Arg Ser Glu Asp Thr Ala Leu Tyr
62              100                 105                 110
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/763,129A

DATE: 04/09/2002
TIME: 12:29:23

Input Set : A:\EP.txt
Output Set: N:\CRF3\04092002\I763129A.raw

```
64 tac tgt gca aga cct ccc tac tat ggt agc tac ggg ggg ttt gct tac        384
65 Tyr Cys Ala Arg Pro Pro Tyr Tyr Gly Ser Tyr Gly Gly Phe Ala Tyr
66         115                 120                 125
68 tgg ggc caa ggg act ctg gtc tct gtc tcg cca                            417
69 Trp Gly Gln Gly Thr Leu Val Ser Val Ser Pro
70         130                 135
73 <210> SEQ ID NO: 2
74 <211> LENGTH: 139
75 <212> TYPE: PRT
76 <213> ORGANISM: Mus musculus
78 <400> SEQUENCE: 2
80 Met Asp Phe Gly Leu Ile Phe Phe Ile Val Ala Leu Leu Lys Gly Val
81 1               5                 10                  15
84 Gln Cys Glu Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Thr
85             20                  25                  30
88 Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser
89         35                  40          r       45
92 Arg Phe Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
93     50                  55                  60
96 Trp Ile Gly Glu Val Asn Pro Asp Asn Asn Thr Met Asn Tyr Thr Pro
97 65                  70                  75                  80
100 Ser Leu Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr
101             85                  90                  95
104 Leu Tyr Leu Gln Met Ser Gln Val Arg Ser Glu Asp Thr Ala Leu Tyr
105             100                 105                 110
108 Tyr Cys Ala Arg Pro Pro Tyr Tyr Gly Ser Tyr Gly Gly Phe Ala Tyr
109             115                 120                 125
112 Trp Gly Gln Gly Thr Leu Val Ser Val Ser Pro
113         130                 135
116 <210> SEQ ID NO: 3
117 <211> LENGTH: 381
118 <212> TYPE: DNA
119 <213> ORGANISM: Mus musculus
121 <220> FEATURE:
122 <221> NAME/KEY: CDS
123 <222> LOCATION: (1)..(381)
124 <223> OTHER INFORMATION:
127 <400> SEQUENCE: 3
128 atg agt gtg ccc act cag gtc ctg ggg ttg ctg ctg ctg tgg ctt aca        48
129 Met Ser Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr
130 1               5                 10                  15
132 gat gcc aga tgt gac atc cag atg act cag tct cca gcc tcc cta tct        96
133 Asp Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
134             20                  25                  30
136 gta tct gtg gga gaa act gtc acc atc aca tgt cga gca agt gag aat        144
137 Val Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn
138         35                  40                  45
140 att tac aat aat tta gct tgg tat cag cag aga cag gga aaa tct cct        192
141 Ile Tyr Asn Asn Leu Ala Trp Tyr Gln Gln Arg Gln Gly Lys Ser Pro
```

```
142     50                  55                  60
144 cag ctc ctg gtc tat gct gca aca aac tta gca gat ggt gtg cca tca     240
145 Gln Leu Leu Val Tyr Ala Ala Thr Asn Leu Ala Asp Gly Val Pro Ser
146 65                  70                  75                  80
148 agg ttc agt ggc agt gga tca ggc aca cag tat tcc ctc aag atc gac     288
149 Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asp
150                 85                  90                  95
152 agc ctg cag tct gaa gat ttt ggg agt tat tac tgt caa cat ttg tgg     336
153 Ser Leu Gln Ser Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Leu Trp
154                 100                 105                 110
156 act tct ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa        381
157 Thr Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
158         115                 120                 125
161 <210> SEQ ID NO: 4
162 <211> LENGTH: 127
163 <212> TYPE: PRT
164 <213> ORGANISM: Mus musculus
166 <400> SEQUENCE: 4
168 Met Ser Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr
169 1               5                   10                  15
172 Asp Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser
173             20                  25                  30
176 Val Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn
177         35                  40                  45
180 Ile Tyr Asn Asn Leu Ala Trp Tyr Gln Gln Arg Gln Gly Lys Ser Pro
181     50                  55                  60
184 Gln Leu Leu Val Tyr Ala Ala Thr Asn Leu Ala Asp Gly Val Pro Ser
185 65                  70                  75                  80
188 Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asp
189                 85                  90                  95
192 Ser Leu Gln Ser Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Leu Trp
193                 100                 105                 110
196 Thr Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
197         115                 120                 125
200 <210> SEQ ID NO: 5
201 <211> LENGTH: 417
202 <212> TYPE: DNA
203 <213> ORGANISM: hybrid
205 <220> FEATURE:
206 <221> NAME/KEY: CDS
207 <222> LOCATION: (1)..(417)
208 <223> OTHER INFORMATION:
211 <400> SEQUENCE: 5
212 atg gat ttt ggg ctg att ttt ttt att gtt gct ctt tta aaa ggg gtc     48
213 Met Asp Phe Gly Leu Ile Phe Phe Ile Val Ala Leu Leu Lys Gly Val
214 1               5                   10                  15
216 cag tgt gag gtg caa ctt gtc gag tct gga ggt gga cta gtg cag cct     96
217 Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
218         20                  25                  30
```

— Invalid response, see error summary sheet item 10

RAW SEQUENCE LISTING   DATE: 04/09/2002
PATENT APPLICATION: US/09/763,129A   TIME: 12:29:23

Input Set : A:\EP.txt
Output Set: N:\CRF3\04092002\I763129A.raw

```
220 gga gga tca ctg aga ctc tcc tgt gca gcc tca gga ttc gat ttt agt       144
221 Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser
222         35                  40                  45
224 aga ttc tgg atg agt tgg gtc cgg cag gct cca ggg aaa ggg ctc gag       192
225 Arg Phe Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
226     50                  55                  60
228 tgg att gga gaa gtt aat cca gat aac aat acg atg aac tat acg cca       240
229 Trp Ile Gly Glu Val Asn Pro Asp Asn Asn Thr Met Asn Tyr Thr Pro
230 65                  70                  75                  80
232 tct cta aag gat aaa ttc acc atc tcc aga gac aac gcc aaa aat acg       288
233 Ser Leu Lys Asp Lys Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr
234                 85                  90                  95
236 ctg tac ctg caa atg aac tca ttg aga gct gag gac acg gcc gtt tac       336
237 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
238             100                 105                 110
240 tac tgt gca aga cct ccc tac tat ggt agc tac ggg ggg ttt gct tac       384
241 Tyr Cys Ala Arg Pro Pro Tyr Tyr Gly Ser Tyr Gly Gly Phe Ala Tyr
242             115                 120                 125
244 tgg ggc caa ggg act ctg gtc acc gtc tcc tca                           417
245 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
246     130                 135
249 <210> SEQ ID NO: 6
250 <211> LENGTH: 139
251 <212> TYPE: PRT
252 <213> ORGANISM: hybrid    - same error
254 <400> SEQUENCE: 6
256 Met Asp Phe Gly Leu Ile Phe Phe Ile Val Ala Leu Leu Lys Gly Val
257 1               5                   10                  15
260 Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
261             20                  25                  30
264 Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser
265         35                  40                  45
268 Arg Phe Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
269     50                  55                  60
272 Trp Ile Gly Glu Val Asn Pro Asp Asn Asn Thr Met Asn Tyr Thr Pro
273 65                  70                  75                  80
276 Ser Leu Lys Asp Lys Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr
277                 85                  90                  95
280 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
281             100                 105                 110
284 Tyr Cys Ala Arg Pro Pro Tyr Tyr Gly Ser Tyr Gly Gly Phe Ala Tyr
285             115                 120                 125
288 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
289     130                 135
292 <210> SEQ ID NO: 7
293 <211> LENGTH: 381
294 <212> TYPE: DNA
295 <213> ORGANISM: hybrid    - same
297 <220> FEATURE:
```

RAW SEQUENCE LISTING   DATE: 04/09/2002
PATENT APPLICATION: US/09/763,129A   TIME: 12:29:23

Input Set : A:\EP.txt
Output Set: N:\CRF3\04092002\I763129A.raw

```
298 <221> NAME/KEY: CDS
299 <222> LOCATION: (1)..(381)
300 <223> OTHER INFORMATION:
303 <400> SEQUENCE: 7
304 atg agt gtg ccc act cag gtc ctg ggg ttg ctg ctg ctg tgg ctt aca        48
305 Met Ser Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr
306 1               5                   10                  15
308 gat gcc aga tgt gac atc cag atg act cag tct cca tcc tcc cta tct        96
309 Asp Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
310             20                  25                  30
312 gca tct gtg gga gac agg gtc acc atc aca tgt cga gca agt gag aat       144
313 Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asn
314             35                  40                  45
316 att tac aat aat tta gct tgg tat cag cag aaa ccg gga aaa gct cct       192
317 Ile Tyr Asn Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
318         50                  55                  60
320 aag cta cta gtc tat gct gca aca aac tta gca gat ggt gtg cca tca       240
321 Lys Leu Leu Val Tyr Ala Ala Thr Asn Leu Ala Asp Gly Val Pro Ser
322 65                  70                  75                  80
324 agg ttc agt ggc agt gga tca ggc aca cag tat acc ctc acg atc agc       288
325 Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Thr Leu Thr Ile Ser
326                 85                  90                  95
328 agc ctc cag cct gag gat ttt gcg act tat tac tgt caa cat ttg tgg       336
329 Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Leu Trp
330             100                 105                 110
332 act tct ccg tac acg ttc gga ggg ggg acc aag gtg gaa ata aaa         381
333 Thr Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
334         115                 120                 125
337 <210> SEQ ID NO: 8
338 <211> LENGTH: 127
339 <212> TYPE: PRT              -same
340 <213> ORGANISM: (hybrid)
342 <400> SEQUENCE: 8
344 Met Ser Val Pro Thr Gln Val Leu Gly Leu Leu Leu Leu Trp Leu Thr
345 1               5                   10                  15
348 Asp Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
349             20                  25                  30
352 Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Asn
353             35                  40                  45
356 Ile Tyr Asn Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
357         50                  55                  60
360 Lys Leu Leu Val Tyr Ala Ala Thr Asn Leu Ala Asp Gly Val Pro Ser
361 65                  70                  75                  80
364 Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Tyr Thr Leu Thr Ile Ser
365                 85                  90                  95
368 Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Leu Trp
369             100                 105                 110
372 Thr Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
373         115                 120                 125
```

VERIFICATION SUMMARY   DATE: 04/09/2002
PATENT APPLICATION: US/09/763,129A   TIME: 12:29:24

Input Set : **A:\EP.txt**
Output Set: **N:\CRF3\04092002\I763129A.raw**

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date